X₁ is any amino acid residue;

X₂ is any amino acid residue;

X₃ is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X₄ is any amino acid residue;

 X_5 is a hydrophobic residue or Gly;

X₆ is a hydrophobic or a hydrophilic residue;

X₇ is Gly, an amide-substituted polar residue or a hydrophobic residue;

X₈ is an amino acid residue other than an aliphatic residue;

X_q is an aliphatic residue;

X₁₀ is any amino acid residue;

 Z_3 is (i) a second peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_4 to X_{10} ;

 Z_4 is the carboxy terminus of the peptide, Z4 having the formula –C(O)OR or –C(O)NRR;

each R is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "-" between residues X_1 through X_{10} , Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" represents a bond.

Claim 2-3 (cancelled)

Claim 4 (previously presented): The compound of claim 1 wherein the compound exhibits antibacterial activity against a Gram-negative bacterium.

Claim 5 (currently amended): An isolated compound which inhibits pilus assembly, said compound comprising SEQ ID NO: 1, wherein the compound is a mimic of a chaperone G₁ beta-strand and the compound exhibits antibacterial

activity against a Gram-negative bacterium. The compound of claim 4 wherein said mimic comprises SEQ ID NO: 1 or an analog thereof.

Claim 6 (cancelled)

Claim 7 (cancelled)

Claim 8 (previously presented): The compound of claim 1 wherein the compound comprises a mimic of an amino terminal motif of a pilus subunit selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 9 (currently amended): The compound of claim 8 wherein said mimic of an amino-terminal motif of a pilus subunit further comprises the amino acid sequence SDVAFRGNLL (SEQ ID NO: 12) or an analog thereof.

Claim 10 (cancelled)

Claim 11 (cancelled)

Claim 12 (cancelled)

Claim 13 (previously presented): The compound of claim 1 wherein one or more of the following conditions are satisfied:

each "-" between residues X_1 through X_{10} , Z_2 and X_1 and X_{10} and Z_3 is an amide linkage;

 Z_1 is H_2N- ;

 Z_4 is -C(O)OH or a salt thereof;

 Z_2 is a bond connecting Z_1 to X_1 ;

 Z_3 is a bond connecting Z_4 to X_{10} ;

 X_1 is an amino acid residue other than a basic residue;

X₂ is an amino acid residue other than an aliphatic residue;

 X_3 is an aliphatic residue or T;

X₄ is an amino acid residue other than an acidic residue;

X₅ is an aliphatic residue, F or G;

X₇ is G, N or A; or

 X_{10} is an aliphatic or a polar residue.

Claim 14 (previously presented): The compound of claim 13 wherein the mimic comprises a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 15 (cancelled)

Claim 16 (currently amended): An isolated compound which inhibits pilus assembly, or a pharmaceutically-acceptable salt thereof, the compound comprising a mimic of a chaperone G₁ beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic is a 7 to 17 residue peptide or peptide analog, having an amino terminus and a carboxy terminus, according to formula (II):

(II)
$$Z_{11} \sim Z_{12} - X_{11} - X_{12} - X_{13} - X_{14} - X_{15} - X_{16} - X_{17} - Z_{13} \sim Z_{14}$$
 or a pharmaceutically-acceptable salt thereof,

wherein:

 Z_{11} is the amino terminus of the peptide, Z_{11} having the formula R'–C(O)–NR'– or R'R'N–;

 Z_{12} is (i) a first peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_{11} to X_{11} ;

X₁₁ is any amino acid residue;

X₁₂ is any amino acid residue;

X₁₃ is a hydrophobic residue;

X₁₄ is any amino acid residue;

X₁₅ is a hydrophobic residue;

X₁₆ is any amino acid residue;

X₁₇ is hydrophobic residue or a hydroxyl-substituted aliphatic residue;

 Z_{13} is (i) a second peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_{14} to X_{17} ;

 Z_{14} is the carboxy terminus of the peptide, Z_{14} having the formula -C(O)OR' or -C(O)NR'R';

each R' is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "-" between residues X_{11} through X_{17} , Z_{12} and X_{11} and X_{17} and Z_{13} independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" independently represents a bond.

Claim 17 (previously presented): The compound of claim 16 wherein one or more of the following conditions are satisfied:

each "-" between residues X_{11} through X_{17} , Z_{12} and X_{11} and X_{17} and Z_{13} is an amide linkage;

 Z_{11} is H_2N_- ;

 Z_{14} is -C(O)OH or a salt thereof;

 Z_{12} is a bond connecting Z_{11} to X_{11} ;

 Z_{13} is a bond connecting Z_{14} to X_{17} ;

X₁₁ is an amino acid residue other than a basic residue;

X₁₃ is an aliphatic residue or M;

X₁₄ is an amino acid residue other than an aromatic residue;

 X_{15} is an aliphatic residue, F or M; and X_{17} is an aliphatic residue, F, M or a hydroxyl-substituted aliphatic residue.

Claim 18 (cancelled)

Claim 19 (currently amended): The compound of any one of claims 1, 2, 5, 8, 9, 13, 14, 16, or 17 wherein said compound exhibits antibacterial activity against one or more Gram-negative bacterium selected from the group consisting of *E. coli*, *H. influenzae*, *S. euteriditis*, *S. typhimurium*, *B. pertussis*, *Y. pestis*, *Y. entarocolitica*, *H. pylori* and *K. pneumoniae*.

Claims 20-135 (cancelled)

Claim 136 (previously presented): An isolated compound which inhibits pilus assembly, the compound consisting of SEQ ID NO: 12.

Claim 137 (previously presented): An isolated compound which inhibits pilus assembly, the compound consisting essentially of SEQ ID NO: 12, wherein the compound is a mimic of an amino terminal motif of a pilus subunit.

Claim 138 (previously presented): An isolated compound which inhibits pilus assembly, the compound comprising a mimic of an amino terminal motif of a pilus subunit, wherein the mimic comprises SEQ ID NO:12.

Claim 139 (previously presented): The compound of claim 138 wherein the compound competitively binds to a pilus subunit hydrophobic groove.

Claim 140-158 (cancelled)

Claim 159 (new) The compound of claim 1 wherein the compound consists essentially of a 10 to 20 residue peptide according to formula (I).